

SEQUENCE LISTING

<110> GARABEDIAN, Michael
TANEJA, Samir
HITTELMAN, Adam
MARKUS, Steven

<120> METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES

<130> GARABEDIAN=1.1A

<140> NOT YET ASSIGNED

<141> 2001-03-26

<150> 60/225,618

<151> 2000-08-15

<150> 60/191,768

<151> 2000-03-24

<160> 20

<170> PatentIn version 3.0

<210> 1

<211> 474

<212> DNA

<213> human

<400> 1

atggcgacgc cccctaagcg gcgggcggtg gaggccacgg gggagaaagt gctgcgctac 60
gagaccttca tcagtgcagt gctgcagcgg gacttgcgaa aggtgctgga ccatcgagac 120
aaggtatatg agcagctggc caaatacatt caactgagaa atgtcattga gcgactccag 180
gaagctaagc actcggagtt atatatgcag gtggatttgg gctgtaactt cttcgttgac 240
acagtgggtcc cagatacttc acgcatttat gtggcccttg gatatggttt tttcctggag 300
ttgacactgg cagaagctct caagttcatt gatcgtgaaga gctctctcct cacagagctc 360
agcaacagcc tcaccaagga ctccatgaat atcaaagccc atatccacat gttgctagag 420
gggcttagag aactacaagg cctgcagaat ttcccagaga agcctcacca ttga 474

<210> 2

<211> 157

<212> PRT

<213> human

<400> 2

Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
1 5 10 15

Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
20 25 30

Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys

35					40					45					
Tyr	Leu	Gln	Leu	Arg	Asn	Val	Ile	Glu	Arg	Leu	Gln	Glu	Ala	Lys	His
50					55					60					
Ser	Glu	Leu	Tyr	Met	Gln	Val	Asp	Leu	Gly	Cys	Asn	Phe	Phe	Val	Asp
65					70					75					80
Thr	Val	Val	Pro	Asp	Thr	Ser	Arg	Ile	Tyr	Val	Ala	Leu	Gly	Tyr	Gly
				85					90					95	
Phe	Phe	Leu	Glu	Leu	Thr	Leu	Ala	Glu	Ala	Leu	Lys	Phe	Ile	Asp	Arg
		100					105						110		
Lys	Ser	Ser	Leu	Leu	Thr	Glu	Leu	Ser	Asn	Ser	Leu	Thr	Lys	Asp	Ser
	115						120					125			
Met	Asn	Ile	Lys	Ala	His	Ile	His	Met	Leu	Leu	Glu	Gly	Leu	Arg	Glu
	130					135					140				
Leu	Gln	Gly	Leu	Gln	Asn	Phe	Pro	Glu	Lys	Pro	His	His			
145					150					155					

<210> 3
 <211> 1097
 <212> DNA
 <213> human

<400> 3
 aaatgcacaa cccggacgga agtgcctctc cgacagcaga tccaggctcg gagctccaga 60
 cgctgggaca ggccgcccgc agaccacccc cgccgcgcgc gggacacgac gccccccgca 120
 ggacacgccc atcagcccgg aaacccttga gctgcttctc ccggaggccg atgcccaccc 180
 gggagcccc aaagactcgc ggctcccggg ggcacctgca tactcaccgc cctgggcctg 240
 ggcccccgct gcagggactg gcgccccgag gcctcaaaac cagcgcccc cgccctccgt 300
 gccagcccca gccgggaccc cacaaggcaa agaccaagaa gattgtgttt gaggatgagt 360
 tgctctccca ggccctcctg ggcgccaaga agcctattgg agccatccct aaggggcata 420
 agcctaggcc ccaccagtg cccgactatg agcttaagta cccgccagtg agcagtgaga 480
 gggaacggag ccgctatgtc gcagtgttcc aggaccagta cggagagttc ttggagctcc 540
 agcacgaggt ggggtgtgca caggcaaagc tcaggcagct ggaggccctg ctgagctccc 600
 tgccccacc ccaaagccag aaggaggccc aagttgcagc ccgggttttg agggagtttg 660
 agatgaagcg aatggatcct ggcttcctgg acaagcaggc tcgctgccac tacctgaagg 720
 gtaaactgag gcatctcaag actcagatcc agaaattcga tgaccaagga gacagcgagg 780
 gctccgtgta cttctaagt cccctgcaga tgggcagagg gatgcatggg gatgcaggtc 840
 ccttgcatctt cttggatatc ctcagctttt cctcttgag ctccccctac caggggtcgc 900
 tttctcctgg attgcaaag cctcttcagt ttggactcag ctctgacagc ccctcctcca 960
 ggaaggcctt ccaggacttc ctctctgagg tcctctagct ctgaccctac agggactcca 1020

gatctcaacc tgttccttg aagtagggcc tgctctccat cccagtga aaacatgta 1080
 ttagacacct aaaaaaa 1097

<210> 4
 <211> 264
 <212> PRT
 <213> Human

<400> 4

Met His Asn Pro Asp Gly Ser Ala Ser Pro Thr Ala Asp Pro Gly Ser
 1 5 10 15
 Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
 20 25 30
 Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
 35 40 45
 Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
 50 55 60
 Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
 65 70 75 80
 Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
 85 90 95
 Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys
 100 105 110
 Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
 115 120 125
 Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
 130 135 140
 Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
 145 150 155 160
 Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
 165 170 175
 Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
 180 185 190
 Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
 195 200 205
 Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
 210 215 220
 Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
 225 230 235 240
 Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
 245 250 255
 Asp Ser Glu Gly Ser Val Tyr Phe
 260

<210> 5
 <211> 517
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <223> n at position 65 is unknown.

<400> 5
 gaacggcacg agggcgcgcc acgcgcggga agcggcgcgcg ggagcgcgcg cggcggggccg 60
 cgcanccgag ggagccgagc gcccgmacgc gcccgagcgg acasacgcca gagccgcgcc 120
 cggggccgag cgcagcgcgcg cggccgssyg ggccgccagg ggcgcgcgcg gcggagcgcg 180
 gggcgcgmgaa aaagggggccc ggcggagacc aagggcaggc gcggcccgcga agggcgccgg 240
 ggaaggcgcc cggcaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac 300
 acacgagcgc gagccgccac aacaccacac cgggcccaag gagaacagca cgccaacgcg 360
 ccagycacgg cgggcacggg aggcggggcca cacacagcgg ccccgccaag gcacggcgca 420
 cggcacaagg gcaccacgcc agacaagcga ggaggcagca cgccgagacc ggccggaggg 480
 ccgcgaccgc cggagaaaag gaacagagag cccccc 517

<210> 6
 <211> 189
 <212> PRT
 <213> Human

<400> 6
 Glu Phe Gly Thr Arg Ala Arg Phe Thr Arg Gly Lys Ser Ala Leu Leu
 1 5 10 15
 Glu Arg Ala Leu Ala Arg Pro Arg Thr Glu Val Ser Leu Ser Ala Phe
 20 25 30
 Ala Leu Leu Ser Pro Ser Trp Tyr Ser Thr Ala Arg Ala Val Phe Ser
 35 40 45
 Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
 50 55 60
 Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
 65 70 75 80
 Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
 85 90 95
 Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
 100 105 110
 Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
 115 120 125
 Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
 130 135 140

Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
145 150 155 160

Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
165 170 175

Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
180 185

<210> 7
<211> 126
<212> DNA
<213> Human

<400> 7
gaattcggca cgaggctcaa gccctacgtg agctacctcg cccctgagag cgaggagacg 60
cccctgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt 120
caagga 126

<210> 8
<211> 42
<212> PRT
<213> Human

<400> 8
Glu Phe Gly Thr Arg Leu Lys Pro Tyr Val Ser Tyr Leu Ala Pro Glu
1 5 10 15
Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
20 25 30
Ala Pro Cys His Arg Lys Gly Leu Gln Gly
35 40

<210> 9
<211> 678
<212> DNA
<213> Human

<220>
<221> misc_feature
<223> n at position 651 is unknown.

<400> 9
gaattcggca cgaggattca ttgccccac aatcctaggc ctaccgcgcg cagtactgat 60
cattctatatt cccctctat tgatccccac ctccaaatat ctcataaca accgactaat 120
caccaccaa caatgactaa tcaaactaac ctcaaaacaa atgataacca tacacaacac 180
taaaggacga acctgatctc ttatactagt atccttaatc atttttattg ccacaactaa 240
cctcctcgga ctctgcctc actcatttac accaaccacc caactatcta taaacctagc 300
catggccatc cccttatgag cgggcgcagt gattataggc tttcgctcta agattaaaaa 360
tgccctagcc cacttcttac cacaaggcac acctacaccc cttatcccca tactagttat 420

```

tatcgaaacc atcagcctac tcattcaacc aatagccctg gccgtacgcc taaccgctaa      480
cattactgca ggccacctac tcatgcacct aattggaagc gccaccctag caatatcaac      540
cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tatectagaa      600
atcgctgtcg ccttaatcca agcctacgtt ttcacacttc tagtaagcct ntactgnacg      660
acaacacata aaaaaaaaaa                                         678

```

```

<210> 10
<211> 60
<212> PRT
<213> Human

```

```
<400> 10
```

```

Glu Phe Gly Thr Arg Ile His Cys Pro His Asn Pro Arg Pro Thr Arg
1           5           10           15
Arg Ser Thr Asp His Ser Ile Ser Pro Ser Ile Asp Pro His Leu Gln
          20           25           30
Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln
          35           40           45
Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His
          50           55           60

```

```

<210> 11
<211> 1918
<212> DNA
<213> Human

```

```

<400> 11
gaattccaat gtggtaaagt cttcgctcaa acatcacaaac ttgcaaggca ttggagagtt      60
catactggag aaaaacctta caagtgtaat gactgtggca gagccttttag tgatcgttca      120
agcctaactt ttcatcaggc aatacatact ggagagaaac cttacaaatg tcatgaatgc      180
ggcaagggtt ttaggcacaa ttcatacctt gcaactcadc ggcgaattca tactggagag      240
aaaccttaca agtgtaatga gtgtgggaaa gccttttagta tgcaattcaaa cctaactacc      300
cataagggtca tccatactgg agagaagcct tacaatgta atcaatgtgg caaggctctc      360
actcagaact cacaccttgc aaatcatcaa aggactcaca ccggagagaa accttaccga      420
tgcaatgagt gtgggaaagc cttcagtgtt cgttcaagcc taaccaccca tcaggcaatc      480
catactggga aaaaacctta caaatgtaat gaatgtggca aggtctttac tcaaaatgct      540
cacctggcaa atcaccgaag aattcatact ggggagaaac cttacaggtg tacagagtgt      600
gggaaagcct ttagggtaag atcaagtcta actaccata tggcaatcca cactggagaa      660
aagcgttaca aatgtaatga gtgtggcaag gtcttcaggc agagttcaaa tcttgcaagt      720
catcacagaa tgcataccgg agagaaacct tacaatgag tgtggtgagg tcattaggta      780

```

```

caattcactc ctttcacatc agttaatttc attcttgaca gaatccttac aaatgtagtg      840
acagtggcca atccctcatg agttgaagca ttaatagata tgagaggcca taagcaagag      900
acatcatgta aacatatgtg gcagagggtc tatccaggcc tcgcagggtta ctaggcatca      960
agatttatat ctttgatgaa acgaaacaaa tgtaatatgc atcctgaggc cattaccag      1020
tgaccgatgg taagtgagga ttcctaggag gaataacagt ctctggtttc cctgtttgcc      1080
tttgatatta tacactgtag aatactcaca agtccaaata tgctaaaaat tatatatattt      1140
taactcacat acgaaaaggt tgcaggatat ttgtaggcag tcagttacct tcaccttatg      1200
aaatgtttca ctgagttatt tgagggtttt tggaagcct actattgcgt ttcaatgtga      1260
actttgaaat cttattgtgc atccttacac accttccatg gtgctttctt ggaaagatca      1320
ttgggatgga aggatcattg attgggtgaa gatcattgat taggtgaagg attatttcta      1380
tccaatttgt gaagaaggag gactttgctt ttaaaattaa gtatcatctg aattagcatt      1440
tgggagtggc gaaaaacaat gtaaaactat gatgtcactc accattctga taatgttcag      1500
ggtgcctttc tcctaccagg agagtactgt ggcttagagg aaagaaatgg tctatcaact      1560
gaacatgaaa tggagcaggc caagacctta ggacattggg atttttgtgg gaggagagta      1620
ataggttaatt agacactgat tgtgtggtag aaatactgca ggggaaaagg tcgccctctt      1680
atgcatcaaa gagcaatacc tgttgtttag caaagagtga tgaaaaattg atcttgtttt      1740
gaaattgaag agagaggcca ggcgcggtgg ctacacctg taatcccagc actttgggag      1800
gctgaggcag gtggatcacc tgaggtcggg agttcgagac cagcctgacc aacatggaga      1860
aaccccaatt gtactaaaaa tacaaaatta gccgggcgtg gtggcaggtg cggaattc      1918

```

```

<210> 12
<211> 252
<212> PRT
<213> Human

```

```
<400> 12
```

```

Glu Phe Gln Cys Gly Lys Val Phe Ala Gln Thr Ser Gln Leu Ala Arg
1          5          10          15
His Trp Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Asp Cys
20          25          30
Gly Arg Ala Phe Ser Asp Arg Ser Ser Leu Thr Phe His Gln Ala Ile
35          40          45
His Thr Gly Glu Lys Pro Tyr Lys Cys His Glu Cys Gly Lys Val Phe
50          55          60
Arg His Asn Ser Tyr Leu Ala Thr His Arg Arg Ile His Thr Gly Glu
65          70          75          80
Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Met His Ser
85          90          95

```

Asn Leu Thr Thr His Lys Val Ile His Thr Gly Glu Lys Pro Tyr Lys
 100 105 110
 Cys Asn Gln Cys Gly Lys Val Phe Thr Gln Asn Ser His Leu Ala Asn
 115 120 125
 His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Asn Glu Cys
 130 135 140
 Gly Lys Ala Phe Ser Val Arg Ser Ser Leu Thr Thr His Gln Ala Ile
 145 150 155 160
 His Thr Gly Lys Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe
 165 170 175
 Thr Gln Asn Ala His Leu Ala Asn His Arg Arg Ile His Thr Gly Glu
 180 185 190
 Lys Pro Tyr Arg Cys Thr Glu Cys Gly Lys Ala Phe Arg Val Arg Ser
 195 200 205
 Ser Leu Thr Thr His Met Ala Ile His Thr Gly Glu Lys Arg Tyr Lys
 210 215 220
 Cys Asn Glu Cys Gly Lys Val Phe Arg Gln Ser Ser Asn Leu Ala Ser
 225 230 235 240
 His His Arg Met His Thr Gly Glu Lys Pro Tyr Lys
 245 250

<210> 13
 <211> 8588
 <212> DNA
 <213> Human

<400> 13
 cgcgccccga gcgcctcttt tcgggattaa aagcgccgcc agctcccgcc gccgcccgcg 60
 tcgccagcag cgccgctgca gccgcccgcg ccggagaagc aaccgctggg cggtgagatc 120
 cccctagaca tgcggctcgg gggcgggcag ctggtgtcag aggagctgat gaacctgggc 180
 gagagcttca tccagaccaa cgaccgctcg ctgaagctct tccagtgcgc cgtctgcaac 240
 aagttcacga cggacaacct ggacatgctg ggctgcaca tgaacgtgga gcgcagcctg 300
 tcggaggacg agtgaaggc ggtgatgggg gactcatacc agtgcaagct ctgccgctac 360
 aacaccagc tcaaggccaa cttccagctg cactgcaaga cagacaagca cgtgcagaag 420
 taccagctgg tggccacat caaggagggc ggcaaggcca acgagtggag gctcaagtgt 480
 gtggccatcg gcaaccccg tgcacctcaag tgcaacgcct gtgactacta caccaacagc 540
 ctggagaagc tgcggctgca cacggtcaac tccaggcacg aggccagcct gaagttgtac 600
 aagcacctgc agcagcatga gagtgggtga gaaggtgaga gctgctacta ccaactgcgtt 660
 ctgtgcaact actccaccaa ggccaagctc aacctcatcc agcatgtgcg ctccatgaag 720
 caccagcgaa gcgagagcct gcgaaagctg cagcggctgc agaagggcct tccagaggag 780

gacgaggacc	tggggcagat	cttcaccatc	cgcaggtgcc	cctccacgga	cccagaagaa	840
gccattgaag	atgttgaagg	accagtgaa	acagctgctg	atccagagga	gcttgctaag	900
gaccaagagg	gcggagcatc	gtccagccaa	gcagagaagg	agctgacaga	ttctcctgca	960
acctccaaac	gcattctcctt	cccaggtagc	tcagagtctc	ccctctcttc	gaagcgacca	1020
aaaacagctg	aggagatcaa	accggagcag	atgtaccagt	gtccctactg	caagtacagt	1080
aatgccgatg	tcaaccggct	ccgggtgcat	gccatgacgc	agcactcggg	gcaacccatg	1140
cttcgctgcc	ccctgtgcca	ggacatgctc	aacaacaaga	tccacctcca	gctgcacctc	1200
acctcacctc	acagcgtggc	acctgactgc	gtggagaagc	tcattatgac	ggtgaccacc	1260
cctgagatgg	tgatgccaa	cagcatgttc	ctcccagcag	ctgttccaga	tcgagatggg	1320
aattccaatt	tggaagaggc	aggaaagcag	cctgaaacct	cagaggatct	gggaaagaac	1380
atcttgccat	ccgcaagcac	agagcaaagc	ggagatttga	aaccatcccc	tgctgaccga	1440
ggctctgtga	gagaagactc	aggcttcac	tgctggaaga	aggggtgcaa	ccagggttttc	1500
aaaacttctg	ctgcccttca	gacgcatttt	aatgaagtgc	atgccaaag	gcctcagctg	1560
ccggtgtcag	atcgccatgt	gtacaagtac	cgctgtaatc	agtgtagcct	ggccttcaag	1620
accattgaaa	agttgcagct	ccattctcag	taccatgtga	tcagagctgc	caccatgtgc	1680
tgtctttgtc	agcgcagttt	ccgaactttc	caggctctga	agaagcacct	tgagacaagc	1740
cacctggagc	tgagtgaggc	tgacatccaa	cagctttatg	gtggcctgct	ggccaatggg	1800
gacctcctgg	caatgggaga	ccccactctg	gctgaggacc	ataccataat	tgttgaggaa	1860
gacaaggagg	aagagagtga	cttggaagat	aaacagagcc	caacgggcag	tgactctggg	1920
tcagtacaag	aagactcggg	ctcagagcca	aagagagctc	tgcccttcag	aaaaggtccc	1980
aattttacta	tggaagagtt	cctagaccct	tctcgccctt	acaagtgtac	cgtctgcaag	2040
gaatctttca	ctcaaaaagaa	tatcctgcta	gtacactaca	attctgtctc	ccacctgcat	2100
aagttaaaga	gagcccttca	agaatcagca	accggtcagc	cagaaccac	cagcagccca	2160
gacaacaaac	cttttaagtg	taacacttgt	aatgtggcct	acagccagag	ttccactctg	2220
gagatccata	tgaggctctgt	gttacatcaa	accaaggccc	gggcagccaa	gctggaggct	2280
gcaagtggca	gcagcaatgg	gactgggaac	agcagcagta	tttccttgag	ctcctccacg	2340
ccaagtctctg	tgagcaccag	tggcagtaac	acctttacca	cctccaatcc	aagcagtgtc	2400
ggcattgctc	caagctctaa	cttactaagc	caagtgccca	ctgagagtgt	agggatgcca	2460
cccctgggga	atcctatttg	tgccaacatt	gcttcccctt	cagagcccaa	agaggccaat	2520
cggaagaaac	tggcagatat	gattgcatcc	aggcagcagc	aacaacagca	gcagcaacag	2580
caacaacaac	aacaacaaca	acaacaaca	gcacaaacgc	tggccagggc	ccagggtcaa	2640
gttcaagctc	acctgcagca	ggagctgcag	caacaggctg	ccctgatcca	gtctcagctg	2700

ttttaacccca ccctccttcc tcacttcccc atgacaactg agaccctgct gcaactacag 2760
 cagcagcagc acctcctctt ccctttctac atccccagtg ctgagttcca gcttaacccc 2820
 gaggtgagct tgccagtgac cagtggggca ctgacactga ctgggacagg cccaggcctg 2880
 ctggaagatc tgaaggctca ggttcaggtc ccacagcaga gccatcagca gatcttgccg 2940
 cagcagcagc agaaccaact ctctatagcc cagagtcact ctgccctcct tcagccaagc 3000
 cagcaccctg aaaagaagaa caaattggtc atcaaagaaa aggaaaaaga aagccagaga 3060
 gagagggaca gcgccgaggg gggagagggc aacaccggtc cgaaggaaac actgccagat 3120
 gccttgaagg ccaaagagaa gaaagagttg gcaccagggg gtggttctga gccttccatg 3180
 ctccctccac gcattgcttc agatgccaga gggaaacgcca ccaaggccct gctggagaac 3240
 tttggctttg agttgggtcat ccagtataat gagaacaagc agaaggtgca gaaaaagaat 3300
 ggggaagactg accagggaga gaacctggaa aagctcgagt gtgactcctg cggaagttg 3360
 ttttccaaca tottgatttt aaagagtcac caagagcacg ttcacagaa ttactttcct 3420
 ttcaaacagc tcgagaggtt tgccaaacag tacagagacc actacgataa actgtaccca 3480
 ctgaggcccc agaccccaga gccaccacca cctccccctc cccccctcc acccccactt 3540
 ccggcagcgc cgctcagcc ggcgtccaca ccagccatcc ccgcatcagc cccaccatc 3600
 acctcaccta caattgcacc ggcccagcca tcagtgccgc tcaccagct ctccatgccg 3660
 atggagctgc ccatcttctc gccgctgatg atgcagacga tgccgctgca gaccttgccg 3720
 gctcagctac ccccgagct gggacctgtg gagcctctgc ctgcggacct ggcccaactc 3780
 taccagcatc agctcaatcc aaccctgctc cagcagcaga acaagaggcc tcgcaccagg 3840
 atcacagatg atcagctccg agtcttgccg caatattttg acattaacaa ctccccagct 3900
 gaagagcaaa taaaagagat ggcagacaag tccgggttgc cccagaaagt gatcaagcac 3960
 tgggttcagga acactctctt caaagagagg cagcgtaaca aggactcccc ttacaacttc 4020
 agtaatcctc ctatcaccag cctggaggag ctcaagattg actcccgcc cccttcgccg 4080
 gaacctcaa agcaggagta ctggggaagc aagaggtctt caagaacaag gtttacggac 4140
 taccagctga gggctttaca ggacttcttc gatgccaatg cttacccaaa ggatgatgaa 4200
 tttgagcaac tctctaattt actgaacctt ccaacccgag tgatagtggg gtggtttcag 4260
 aatgcccagc agaaggccag gaagaattat gagaatcagg gagagggcaa agatggagag 4320
 cggcgtgagc ttacaaatga tagatacatt cgaacaagca acttgaacta ccagtgcaaa 4380
 aaatgtagcc tgggtgtttca gcgcatcttt gatctcatca agcaccagaa gaagctgtgt 4440
 tacaaggatg aggatgagga ggggcaggac gacagccaaa atgaggattc catggatgcc 4500
 atggaaatcc tgacgcctac cagctcatcc tgcagtaccc cgatgccctc acaggcttac 4560

agcgccccag caccatcagc caataatata gcttctctcg ctttcttgca gcttacagcg 4620
 gaggctgagg aactggccac cttcaattca aaaacagagg caggcgatga gaaaccaaag 4680
 ctggcggaag ctcccagtg cagaccaaac caaacccaag aaaagcaagg acaaccaaag 4740
 ccagagctgc agcagcaaga gcagcccgag cagaagacca aactccccca gcagaagctc 4800
 cccagctgg tgtccctgcc ttcgttgcca cagcctctc cacaagcgcc cctccacag 4860
 tgccccttac cccagtcgag cccagtcct tcccagctct cccacctgcc cctcaagccc 4920
 ctccacacat caactcctca acagctcgca aacctacctc ctcagctaata cccctaccag 4980
 tgtgaccagt gtaagttggc atttccgtca tttgagcact ggcaggagca tcagcagctc 5040
 cacttctga gcgcgcagaa ccagttcatc ccccccaagt ttttgagcag gtccctggat 5100
 atgcctttca tgctctttga tcccagtaac ccactcctgg ccagccagct gctctctggg 5160
 gccatactc agattccagc aagctcagcc acttctcctt caactccaac ctccacaatg 5220
 aacactctca agaggaagct ggaggaaaag gccagtgaac gccctggcga aaacgacagt 5280
 gggacaggag gagaagagcc tcagagagac aagcgtttga gaacaaccat cacaccggaa 5340
 caactagaaa ttctctacca gaagtatcta ctggattcca atccgactcg aaagatgttg 5400
 gatcacattg cacacgaggt gggcttgaag aaacgtgtgg tacaagtctg gtttcagaac 5460
 acccgagctc gggaaaggaa aggacagttc cgggctgtag gccagcgca ggccacagg 5520
 agatgccctt tttgcagagc gctcttcaaa gccaagactg ctcttgaggc tcatatccgg 5580
 tcccgtcact ggcatgaagc caagagagct ggctacaacc taactctgtc tgcgatgctc 5640
 ttagactgtg atgggggact ccagatgaaa ggagatattt ttgacggaac tagcttttcc 5700
 cacctacccc caagcagtag tgatggctag ggtgtcccc tctcacctgt gagtaaaacc 5760
 atggaattgt caccagaac tcttctaagc ccttctcca ttaagggtga agggattgaa 5820
 gactttgaaa gccctccat gtctcagtt aatctaaact ttgaccaaac taagctggac 5880
 aacgatgact gttcctctgt caacacagca atcacagata ccacaactgg agacgagggc 5940
 aacgcagata acgacagtg aacgggaata gcaactgaaa ccaaactctc ttctgcaccc 6000
 aacgaagggt tgaccaaagc ggccatgatg gcaatgtctg agtatgaaga tcggttgta 6060
 tctggtctgg tcagcccggc cccgagcttt tatagcaagg aatatgacaa tgaaggatca 6120
 gtggactaca gtgaaacctc aagccttgca gatccctgct ccccgagtcc tgggtgcgagt 6180
 ggatctgcag gcaaatctgg tgacagcggg gatcggcctg ggcagaaacg ttttcgcact 6240
 caaatgacca atctgcagct gaaggtcctc aagtcagtct ttaatgacta caggacaccc 6300
 actatgctag aatgtgaggt cctgggcaat gacattggac tgccaaagag agtcgttcag 6360
 gtctggttcc agaatgcccg ggcaaaagaa aagaagtcca agttaagcat ggccaagcat 6420
 tttggtataa accaaacgag ttatgagga cccaaaacag agtgcacttt gtgtggcatc 6480

aagtacagcg ctcggctgtc tgtacgtgac catatctttt cccaacagca tatctccaaa 6540
gttaaagaca ccattggaag ccagctggac aaggagaaag aatactttga cccagccacc 6600
gtacgtcagt tgatggctca acaagagttg gaccggatta aaaaggccaa cgaggtcctt 6660
ggactggcag ctcagcagca agggatgttt gacaacaccc ctcttcaggc ccttaacctt 6720
cctacagcat atccagcgct ccagggcatt cctcctgtgt tgctcccggg cctcaacagc 6780
ccctccttgc caggctttac tccatccaac acagctttaa cgtctcctaa gccgaacttg 6840
atgggtctgc ccagcacaac tgttccttcc cctggcctcc ccacttctgg attaccaaat 6900
aaaccgtcct cagcgtcgct gagtcccca accccagcac aagccacgat ggcgatgggc 6960
cctcagcaac cccccagca gcagcagcag cagcagcaac cacagggtgca gcagcctccc 7020
ccgccgccag cagcccagcc gccaccaca ccacagctcc cactgcaaca gcagcagcaa 7080
cgcaaggaca aagacagtga gaaagtaaag gagaaggaaa aggacacaaa agggaaaggg 7140
gaacccttgc ctgtcccca gaaggagaaa ggagaggccc ccacggcaac tgcagccacg 7200
atctcagccc cgctgcccac catggagtat gcggtagacc ctgcacagct gcaggccctg 7260
caggcccgct tgacttcgga cccacagca ttgctcaca gccagttcct tccttacttt 7320
gtaccaggct tttctcctta ttatgtctcc cagatccctg gcgccctgca gagcgggtac 7380
ctgcagccta tgtatggcat ggaaggcctg tccccctaca gccctgcact gtcgcaggcc 7440
ctgatggggc tgtccccagg ctccctactg cagcagtacc agcaatacca gcagagtctg 7500
caggaggcaa ttcagcagca gcagcagcaa aaagtgcagc agcagcagcc caaagcaagc 7560
caaaccocag tcccccccg ggctccttcc ccagacaaaag accctgccaa agaatcccc 7620
aaaccagaag aacagaaaaa cccccccgt gaggtgtccc ccctcctgcc gaaactccct 7680
gaagagccag aagcagaaa gaaaagtgcg gactccctct acgaccctt cattgttcca 7740
aaggtgcagt acaagttggc ctgccgcaag tgccaggcgg gcttcagcga cgaggaggca 7800
gcgaggagcc acctgaagtc cctctgtctt ttcggccagt ctgtggtgaa cctgcaagag 7860
atggtgcttc acgtccccac cggcggcggc ggcggtggca gtggcggcgg cggcggcgg 7920
ggcggcggcg gcggcggcgg cggcggcggc tcgtaccact gcctggcgtg cgagagcgcg 7980
ctctgtgggg aggaagctct gagtcaacat ctcgagtcgg ccttgcaaca acacagaaca 8040
atcacgagag cagcaagaaa cgccaaagag caccctagtt tattacctca ctctgcctgc 8100
ttccccgac ctagcaccgc atctacctcg cagtctgcgg ctactcaaa cgacagcccc 8160
cctccccctg cggcggcggc cccctcctcc gcttcccccc acgcctccag gaagtcttgg 8220
ccgcaagtgg tctcccgggc ttcggcagcg aagccccctt ctttctctcc tctctcctca 8280
tcttcaacgg ttacctcaag ttcattgcag acctcagggg ttcagccctc gatgccaaca 8340

gacgactatt cggaggagtc tgacacggat ctcagccaaa agtccgacgg accggcgagc 8400
 ccggtggagg gtcccaaaga cccagctgc cccaaggaca gtggtctgac cagtgtagga 8460
 acggacacct tcagattgta agctttgaag atgaacaata caaacaatg aatttaaata 8520
 caaaaattaa taacaaacca atttcaaaaa tagactaact gcaattccaa agcttctaac 8580
 caaaaaaac 8588

<210> 14
 <211> 2783
 <212> PRT
 <213> Human

<400> 14

Met Arg Leu Gly Gly Gly Gln Leu Val Ser Glu Glu Leu Met Asn Leu
 1 5 10 15
 Gly Glu Ser Phe Ile Gln Thr Asn Asp Pro Ser Leu Lys Leu Phe Gln
 20 25 30
 Cys Ala Val Cys Asn Lys Phe Thr Thr Asp Asn Leu Asp Met Leu Gly
 35 40 45
 Leu His Met Asn Val Glu Arg Ser Leu Ser Glu Asp Glu Trp Lys Ala
 50 55 60
 Val Met Gly Asp Ser Tyr Gln Cys Lys Leu Cys Arg Tyr Asn Thr Gln
 65 70 75 80
 Leu Lys Ala Asn Phe Gln Leu His Cys Lys Thr Asp Lys His Val Gln
 85 90 95
 Lys Tyr Gln Leu Val Ala His Ile Lys Glu Gly Gly Lys Ala Asn Glu
 100 105 110
 Trp Arg Leu Lys Cys Val Ala Ile Gly Asn Pro Val His Leu Lys Cys
 115 120 125
 Asn Ala Cys Asp Tyr Tyr Thr Asn Ser Leu Glu Lys Leu Arg Leu His
 130 135 140
 Thr Val Asn Ser Arg His Glu Ala Ser Leu Lys Leu Tyr Lys His Leu
 145 150 155 160
 Gln Gln His Glu Ser Gly Val Glu Gly Glu Ser Cys Tyr Tyr His Cys
 165 170 175
 Val Leu Cys Asn Tyr Ser Thr Lys Ala Lys Leu Asn Leu Ile Gln His
 180 185 190
 Val Arg Ser Met Lys His Gln Arg Ser Glu Ser Leu Arg Lys Leu Gln
 195 200 205
 Arg Leu Gln Lys Gly Leu Pro Glu Glu Asp Glu Asp Leu Gly Gln Ile
 210 215 220
 Phe Thr Ile Arg Arg Cys Pro Ser Thr Asp Pro Glu Glu Ala Ile Glu
 225 230 235 240

Asp	Val	Glu	Gly	Pro	Ser	Glu	Thr	Ala	Ala	Asp	Pro	Glu	Glu	Leu	Ala	245	250	255
Lys	Asp	Gln	Glu	Gly	Gly	Ala	Ser	Ser	Ser	Gln	Ala	Glu	Lys	Glu	Leu	260	265	270
Thr	Asp	Ser	Pro	Ala	Thr	Ser	Lys	Arg	Ile	Ser	Phe	Pro	Gly	Ser	Ser	275	280	285
Glu	Ser	Pro	Leu	Ser	Ser	Lys	Arg	Pro	Lys	Thr	Ala	Glu	Glu	Ile	Lys	290	295	300
Pro	Glu	Gln	Met	Tyr	Gln	Cys	Pro	Tyr	Cys	Lys	Tyr	Ser	Asn	Ala	Asp	305	310	315
Val	Asn	Arg	Leu	Arg	Val	His	Ala	Met	Thr	Gln	His	Ser	Val	Gln	Pro	325	330	335
Met	Leu	Arg	Cys	Pro	Leu	Cys	Gln	Asp	Met	Leu	Asn	Asn	Lys	Ile	His	340	345	350
Leu	Gln	Leu	His	Leu	Thr	His	Leu	His	Ser	Val	Ala	Pro	Asp	Cys	Val	355	360	365
Glu	Lys	Leu	Ile	Met	Thr	Val	Thr	Thr	Pro	Glu	Met	Val	Met	Pro	Ser	370	375	380
Ser	Met	Phe	Leu	Pro	Ala	Ala	Val	Pro	Asp	Arg	Asp	Gly	Asn	Ser	Asn	385	390	395
Leu	Glu	Glu	Ala	Gly	Lys	Gln	Pro	Glu	Thr	Ser	Glu	Asp	Leu	Gly	Lys	405	410	415
Asn	Ile	Leu	Pro	Ser	Ala	Ser	Thr	Glu	Gln	Ser	Gly	Asp	Leu	Lys	Pro	420	425	430
Ser	Pro	Ala	Asp	Pro	Gly	Ser	Val	Arg	Glu	Asp	Ser	Gly	Phe	Ile	Cys	435	440	445
Trp	Lys	Lys	Gly	Cys	Asn	Gln	Val	Phe	Lys	Thr	Ser	Ala	Ala	Leu	Gln	450	455	460
Thr	His	Phe	Asn	Glu	Val	His	Ala	Lys	Arg	Pro	Gln	Leu	Pro	Val	Ser	465	470	475
Asp	Arg	His	Val	Tyr	Lys	Tyr	Arg	Cys	Asn	Gln	Cys	Ser	Leu	Ala	Phe	485	490	495
Lys	Thr	Ile	Glu	Lys	Leu	Gln	Leu	His	Ser	Gln	Tyr	His	Val	Ile	Arg	500	505	510
Ala	Ala	Thr	Met	Cys	Cys	Leu	Cys	Gln	Arg	Ser	Phe	Arg	Thr	Phe	Gln	515	520	525
Ala	Leu	Lys	Lys	His	Leu	Glu	Thr	Ser	His	Leu	Glu	Leu	Ser	Glu	Ala	530	535	540
Asp	Ile	Gln	Gln	Leu	Tyr	Gly	Gly	Leu	Leu	Ala	Asn	Gly	Asp	Leu	Leu	545	550	555
Ala	Met	Gly	Asp	Pro	Thr	Leu	Ala	Glu	Asp	His	Thr	Ile	Ile	Val	Glu	565	570	575

Glu Asp Lys Glu Glu Glu Ser Asp Leu Glu Asp Lys Gln Ser Pro Thr
 580 585 590
 Gly Ser Asp Ser Gly Ser Val Gln Glu Asp Ser Gly Ser Glu Pro Lys
 595 600 605
 Arg Ala Leu Pro Phe Arg Lys Gly Pro Asn Phe Thr Met Glu Lys Phe
 610 615 620
 Leu Asp Pro Ser Arg Pro Tyr Lys Cys Thr Val Cys Lys Glu Ser Phe
 625 630 635 640
 Thr Gln Lys Asn Ile Leu Leu Val His Tyr Asn Ser Val Ser His Leu
 645 650 655
 His Lys Leu Lys Arg Ala Leu Gln Glu Ser Ala Thr Gly Gln Pro Glu
 660 665 670
 Pro Thr Ser Ser Pro Asp Asn Lys Pro Phe Lys Cys Asn Thr Cys Asn
 675 680 685
 Val Ala Tyr Ser Gln Ser Ser Thr Leu Glu Ile His Met Arg Ser Val
 690 695 700
 Leu His Gln Thr Lys Ala Arg Ala Ala Lys Leu Glu Ala Ala Ser Gly
 705 710 715 720
 Ser Ser Asn Gly Thr Gly Asn Ser Ser Ser Ile Ser Leu Ser Ser Ser
 725 730 735
 Thr Pro Ser Pro Val Ser Thr Ser Gly Ser Asn Thr Phe Thr Thr Ser
 740 745 750
 Asn Pro Ser Ser Ala Gly Ile Ala Pro Ser Ser Asn Leu Leu Ser Gln
 755 760 765
 Val Pro Thr Glu Ser Val Gly Met Pro Pro Leu Gly Asn Pro Ile Gly
 770 775 780
 Ala Asn Ile Ala Ser Pro Ser Glu Pro Lys Glu Ala Asn Arg Lys Lys
 785 790 795 800
 Leu Ala Asp Met Ile Ala Ser Arg Gln Gln Gln Gln Gln Gln Gln
 805 810 815
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Gln Thr Leu Ala
 820 825 830
 Gln Ala Gln Ala Gln Val Gln Ala His Leu Gln Gln Glu Leu Gln Gln
 835 840 845
 Gln Ala Ala Leu Ile Gln Ser Gln Leu Phe Asn Pro Thr Leu Leu Pro
 850 855 860
 His Phe Pro Met Thr Thr Glu Thr Leu Leu Gln Leu Gln Gln Gln Gln
 865 870 875 880
 His Leu Leu Phe Pro Phe Tyr Ile Pro Ser Ala Glu Phe Gln Leu Asn
 885 890 895
 Pro Glu Val Ser Leu Pro Val Thr Ser Gly Ala Leu Thr Leu Thr Gly
 900 905 910

Thr Gly Pro Gly Leu Leu Glu Asp Leu Lys Ala Gln Val Gln Val Pro
 915 920 925
 Gln Gln Ser His Gln Gln Ile Leu Pro Gln Gln Gln Gln Asn Gln Leu
 930 935 940
 Ser Ile Ala Gln Ser His Ser Ala Leu Leu Gln Pro Ser Gln His Pro
 945 950 955 960
 Glu Lys Lys Asn Lys Leu Val Ile Lys Glu Lys Glu Lys Glu Ser Gln
 965 970 975
 Arg Glu Arg Asp Ser Ala Glu Gly Gly Glu Gly Asn Thr Gly Pro Lys
 980 985 990
 Glu Thr Leu Pro Asp Ala Leu Lys Ala Lys Glu Lys Lys Glu Leu Ala
 995 1000 1005
 Pro Gly Gly Gly Ser Glu Pro Ser Met Leu Pro Pro Arg Ile Ala
 1010 1015 1020
 Ser Asp Ala Arg Gly Asn Ala Thr Lys Ala Leu Leu Glu Asn Phe
 1025 1030 1035
 Gly Phe Glu Leu Val Ile Gln Tyr Asn Glu Asn Lys Gln Lys Val
 1040 1045 1050
 Gln Lys Lys Asn Gly Lys Thr Asp Gln Gly Glu Asn Leu Glu Lys
 1055 1060 1065
 Leu Glu Cys Asp Ser Cys Gly Lys Leu Phe Ser Asn Ile Leu Ile
 1070 1075 1080
 Leu Lys Ser His Gln Glu His Val His Gln Asn Tyr Phe Pro Phe
 1085 1090 1095
 Lys Gln Leu Glu Arg Phe Ala Lys Gln Tyr Arg Asp His Tyr Asp
 1100 1105 1110
 Lys Leu Tyr Pro Leu Arg Pro Gln Thr Pro Glu Pro Pro Pro Pro
 1115 1120 1125
 Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Ala Ala Pro Pro Gln
 1130 1135 1140
 Pro Ala Ser Thr Pro Ala Ile Pro Ala Ser Ala Pro Pro Ile Thr
 1145 1150 1155
 Ser Pro Thr Ile Ala Pro Ala Gln Pro Ser Val Pro Leu Thr Gln
 1160 1165 1170
 Leu Ser Met Pro Met Glu Leu Pro Ile Phe Ser Pro Leu Met Met
 1175 1180 1185
 Gln Thr Met Pro Leu Gln Thr Leu Pro Ala Gln Leu Pro Pro Gln
 1190 1195 1200
 Leu Gly Pro Val Glu Pro Leu Pro Ala Asp Leu Ala Gln Leu Tyr
 1205 1210 1215
 Gln His Gln Leu Asn Pro Thr Leu Leu Gln Gln Gln Asn Lys Arg
 1220 1225 1230

Pro	Arg	Thr	Arg	Ile	Thr	Asp	Asp	Gln	Leu	Arg	Val	Leu	Arg	Gln
1235						1240					1245			
Tyr	Phe	Asp	Ile	Asn	Asn	Ser	Pro	Ser	Glu	Glu	Gln	Ile	Lys	Glu
1250						1255					1260			
Met	Ala	Asp	Lys	Ser	Gly	Leu	Pro	Gln	Lys	Val	Ile	Lys	His	Trp
1265						1270					1275			
Phe	Arg	Asn	Thr	Leu	Phe	Lys	Glu	Arg	Gln	Arg	Asn	Lys	Asp	Ser
1280						1285					1290			
Pro	Tyr	Asn	Phe	Ser	Asn	Pro	Pro	Ile	Thr	Ser	Leu	Glu	Glu	Leu
1295						1300					1305			
Lys	Ile	Asp	Ser	Arg	Pro	Pro	Ser	Pro	Glu	Pro	Pro	Lys	Gln	Glu
1310						1315					1320			
Tyr	Trp	Gly	Ser	Lys	Arg	Ser	Ser	Arg	Thr	Arg	Phe	Thr	Asp	Tyr
1325						1330					1335			
Gln	Leu	Arg	Val	Leu	Gln	Asp	Phe	Phe	Asp	Ala	Asn	Ala	Tyr	Pro
1340						1345					1350			
Lys	Asp	Asp	Glu	Phe	Glu	Gln	Leu	Ser	Asn	Leu	Leu	Asn	Leu	Pro
1355						1360					1365			
Thr	Arg	Val	Ile	Val	Val	Trp	Phe	Gln	Asn	Ala	Arg	Gln	Lys	Ala
1370						1375					1380			
Arg	Lys	Asn	Tyr	Glu	Asn	Gln	Gly	Glu	Gly	Lys	Asp	Gly	Glu	Arg
1385						1390					1395			
Arg	Glu	Leu	Thr	Asn	Asp	Arg	Tyr	Ile	Arg	Thr	Ser	Asn	Leu	Asn
1400						1405					1410			
Tyr	Gln	Cys	Lys	Lys	Cys	Ser	Leu	Val	Phe	Gln	Arg	Ile	Phe	Asp
1415						1420					1425			
Leu	Ile	Lys	His	Gln	Lys	Lys	Leu	Cys	Tyr	Lys	Asp	Glu	Asp	Glu
1430						1435					1440			
Glu	Gly	Gln	Asp	Asp	Ser	Gln	Asn	Glu	Asp	Ser	Met	Asp	Ala	Met
1445						1450					1455			
Glu	Ile	Leu	Thr	Pro	Thr	Ser	Ser	Ser	Cys	Ser	Thr	Pro	Met	Pro
1460						1465					1470			
Ser	Gln	Ala	Tyr	Ser	Ala	Pro	Ala	Pro	Ser	Ala	Asn	Asn	Thr	Ala
1475						1480					1485			
Ser	Ser	Ala	Phe	Leu	Gln	Leu	Thr	Ala	Glu	Ala	Glu	Glu	Leu	Ala
1490						1495					1500			
Thr	Phe	Asn	Ser	Lys	Thr	Glu	Ala	Gly	Asp	Glu	Lys	Pro	Lys	Leu
1505						1510					1515			
Ala	Glu	Ala	Pro	Ser	Ala	Gln	Pro	Asn	Gln	Thr	Gln	Glu	Lys	Gln
1520						1525					1530			
Gly	Gln	Pro	Lys	Pro	Glu	Leu	Gln	Gln	Gln	Glu	Gln	Pro	Glu	Gln
1535						1540					1545			

Lys Thr	Asn Thr	Pro Gln	Gln	Lys Leu	Pro Gln	Leu	Val Ser	Leu	
1550			1555			1560			
Pro Ser	Leu Pro	Gln Pro	Pro	Pro Gln	Ala Pro	Pro	Pro Gln	Cys	
1565			1570			1575			
Pro Leu	Pro Gln	Ser Ser	Pro	Ser Pro	Ser Gln	Leu	Ser His	Leu	
1580			1585			1590			
Pro Leu	Lys Pro	Leu His	Thr	Ser Thr	Pro Gln	Gln	Leu Ala	Asn	
1595			1600			1605			
Leu Pro	Pro Gln	Leu Ile	Pro	Tyr Gln	Cys Asp	Gln	Cys Lys	Leu	
1610			1615			1620			
Ala Phe	Pro Ser	Phe Glu	His	Trp Gln	Glu His	Gln	Gln Leu	His	
1625			1630			1635			
Phe Leu	Ser Ala	Gln Asn	Gln	Phe Ile	His Pro	Gln	Phe Leu	Asp	
1640			1645			1650			
Arg Ser	Leu Asp	Met Pro	Phe	Met Leu	Phe Asp	Pro	Ser Asn	Pro	
1655			1660			1665			
Leu Leu	Ala Ser	Gln Leu	Leu	Ser Gly	Ala Ile	Pro	Gln Ile	Pro	
1670			1675			1680			
Ala Ser	Ser Ala	Thr Ser	Pro	Ser Thr	Pro Thr	Ser	Thr Met	Asn	
1685			1690			1695			
Thr Leu	Lys Arg	Lys Leu	Glu	Glu Lys	Ala Ser	Ala	Ser Pro	Gly	
1700			1705			1710			
Glu Asn	Asp Ser	Gly Thr	Gly	Gly Glu	Glu Pro	Gln	Arg Asp	Lys	
1715			1720			1725			
Arg Leu	Arg Thr	Thr Ile	Thr	Pro Glu	Gln Leu	Glu	Ile Leu	Tyr	
1730			1735			1740			
Gln Lys	Tyr Leu	Leu Asp	Ser	Asn Pro	Thr Arg	Lys	Met Leu	Asp	
1745			1750			1755			
His Ile	Ala His	Glu Val	Gly	Leu Lys	Lys Arg	Val	Val Gln	Val	
1760			1765			1770			
Trp Phe	Gln Asn	Thr Arg	Ala	Arg Glu	Arg Lys	Gly	Gln Phe	Arg	
1775			1780			1785			
Ala Val	Gly Pro	Ala Gln	Ala	His Arg	Arg Cys	Pro	Phe Cys	Arg	
1790			1795			1800			
Ala Leu	Phe Lys	Ala Lys	Thr	Ala Leu	Glu Ala	His	Ile Arg	Ser	
1805			1810			1815			
Arg His	Trp His	Glu Ala	Lys	Arg Ala	Gly Tyr	Asn	Leu Thr	Leu	
1820			1825			1830			
Ser Ala	Met Leu	Leu Asp	Cys	Asp Gly	Gly Leu	Gln	Met Lys	Gly	
1835			1840			1845			
Asp Ile	Phe Asp	Gly Thr	Ser	Phe Ser	His Leu	Pro	Pro Ser	Ser	
1850			1855			1860			

Ser	Asp	Gly	Gln	Gly	Val	Pro	Leu	Ser	Pro	Val	Ser	Lys	Thr	Met
1865						1870					1875			
Glu	Leu	Ser	Pro	Arg	Thr	Leu	Leu	Ser	Pro	Ser	Ser	Ile	Lys	Val
1880						1885					1890			
Glu	Gly	Ile	Glu	Asp	Phe	Glu	Ser	Pro	Ser	Met	Ser	Ser	Val	Asn
1895						1900					1905			
Leu	Asn	Phe	Asp	Gln	Thr	Lys	Leu	Asp	Asn	Asp	Asp	Cys	Ser	Ser
1910						1915					1920			
Val	Asn	Thr	Ala	Ile	Thr	Asp	Thr	Thr	Thr	Gly	Asp	Glu	Gly	Asn
1925						1930					1935			
Ala	Asp	Asn	Asp	Ser	Ala	Thr	Gly	Ile	Ala	Thr	Glu	Thr	Lys	Ser
1940						1945					1950			
Ser	Ser	Ala	Pro	Asn	Glu	Gly	Leu	Thr	Lys	Ala	Ala	Met	Met	Ala
1955						1960					1965			
Met	Ser	Glu	Tyr	Glu	Asp	Arg	Leu	Ser	Ser	Gly	Leu	Val	Ser	Pro
1970						1975					1980			
Ala	Pro	Ser	Phe	Tyr	Ser	Lys	Glu	Tyr	Asp	Asn	Glu	Gly	Thr	Val
1985						1990					1995			
Asp	Tyr	Ser	Glu	Thr	Ser	Ser	Leu	Ala	Asp	Pro	Cys	Ser	Pro	Ser
2000						2005					2010			
Pro	Gly	Ala	Ser	Gly	Ser	Ala	Gly	Lys	Ser	Gly	Asp	Ser	Gly	Asp
2015						2020					2025			
Arg	Pro	Gly	Gln	Lys	Arg	Phe	Arg	Thr	Gln	Met	Thr	Asn	Leu	Gln
2030						2035					2040			
Leu	Lys	Val	Leu	Lys	Ser	Cys	Phe	Asn	Asp	Tyr	Arg	Thr	Pro	Thr
2045						2050					2055			
Met	Leu	Glu	Cys	Glu	Val	Leu	Gly	Asn	Asp	Ile	Gly	Leu	Pro	Lys
2060						2065					2070			
Arg	Val	Val	Gln	Val	Trp	Phe	Gln	Asn	Ala	Arg	Ala	Lys	Glu	Lys
2075						2080					2085			
Lys	Ser	Lys	Leu	Ser	Met	Ala	Lys	His	Phe	Gly	Ile	Asn	Gln	Thr
2090						2095					2100			
Ser	Tyr	Glu	Gly	Pro	Lys	Thr	Glu	Cys	Thr	Leu	Cys	Gly	Ile	Lys
2105						2110					2115			
Tyr	Ser	Ala	Arg	Leu	Ser	Val	Arg	Asp	His	Ile	Phe	Ser	Gln	Gln
2120						2125					2130			
His	Ile	Ser	Lys	Val	Lys	Asp	Thr	Ile	Gly	Ser	Gln	Leu	Asp	Lys
2135						2140					2145			
Glu	Lys	Glu	Tyr	Phe	Asp	Pro	Ala	Thr	Val	Arg	Gln	Leu	Met	Ala
2150						2155					2160			
Gln	Gln	Glu	Leu	Asp	Arg	Ile	Lys	Lys	Ala	Asn	Glu	Val	Leu	Gly
2165						2170					2175			

Leu	Ala	Ala	Gln	Gln	Gln	Gly	Met	Phe	Asp	Asn	Thr	Pro	Leu	Gln
2180						2185					2190			
Ala	Leu	Asn	Leu	Pro	Thr	Ala	Tyr	Pro	Ala	Leu	Gln	Gly	Ile	Pro
2195						2200					2205			
Pro	Val	Leu	Leu	Pro	Gly	Leu	Asn	Ser	Pro	Ser	Leu	Pro	Gly	Phe
2210						2215					2220			
Thr	Pro	Ser	Asn	Thr	Ala	Leu	Thr	Ser	Pro	Lys	Pro	Asn	Leu	Met
2225						2230					2235			
Gly	Leu	Pro	Ser	Thr	Thr	Val	Pro	Ser	Pro	Gly	Leu	Pro	Thr	Ser
2240						2245					2250			
Gly	Leu	Pro	Asn	Lys	Pro	Ser	Ser	Ala	Ser	Leu	Ser	Ser	Pro	Thr
2255						2260					2265			
Pro	Ala	Gln	Ala	Thr	Met	Ala	Met	Gly	Pro	Gln	Gln	Pro	Pro	Gln
2270						2275					2280			
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Val	Gln	Gln	Pro	Pro	Pro
2285						2290					2295			
Pro	Pro	Ala	Ala	Gln	Pro	Pro	Pro	Thr	Pro	Gln	Leu	Pro	Leu	Gln
2300						2305					2310			
Gln	Gln	Gln	Gln	Arg	Lys	Asp	Lys	Asp	Ser	Glu	Lys	Val	Lys	Glu
2315						2320					2325			
Lys	Glu	Lys	Ala	His	Lys	Gly	Lys	Gly	Glu	Pro	Leu	Pro	Val	Pro
2330						2335					2340			
Lys	Lys	Glu	Lys	Gly	Glu	Ala	Pro	Thr	Ala	Thr	Ala	Ala	Thr	Ile
2345						2350					2355			
Ser	Ala	Pro	Leu	Pro	Thr	Met	Glu	Tyr	Ala	Val	Asp	Pro	Ala	Gln
2360						2365					2370			
Leu	Gln	Ala	Leu	Gln	Ala	Ala	Leu	Thr	Ser	Asp	Pro	Thr	Ala	Leu
2375						2380					2385			
Leu	Thr	Ser	Gln	Phe	Leu	Pro	Tyr	Phe	Val	Pro	Gly	Phe	Ser	Pro
2390						2395					2400			
Tyr	Tyr	Ala	Pro	Gln	Ile	Pro	Gly	Ala	Leu	Gln	Ser	Gly	Tyr	Leu
2405						2410					2415			
Gln	Pro	Met	Tyr	Gly	Met	Glu	Gly	Leu	Phe	Pro	Tyr	Ser	Pro	Ala
2420						2425					2430			
Leu	Ser	Gln	Ala	Leu	Met	Gly	Leu	Ser	Pro	Gly	Ser	Leu	Leu	Gln
2435						2440					2445			
Gln	Tyr	Gln	Gln	Tyr	Gln	Gln	Ser	Leu	Gln	Glu	Ala	Ile	Gln	Gln
2450						2455					2460			
Gln	Gln	Gln	Gln	Lys	Val	Gln	Gln	Gln	Gln	Pro	Lys	Ala	Ser	Gln
2465						2470					2475			
Thr	Pro	Val	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Asp	Lys	Asp	Pro	Ala
2480						2485					2490			

```

Lys Glu Ser Pro Lys Pro Glu Glu Gln Lys Asn Thr Pro Arg Glu
2495 2500 2505
Val Ser Pro Leu Leu Pro Lys Leu Pro Glu Glu Pro Glu Ala Glu
2510 2515 2520
Ser Lys Ser Ala Asp Ser Leu Tyr Asp Pro Phe Ile Val Pro Lys
2525 2530 2535
Val Gln Tyr Lys Leu Val Cys Arg Lys Cys Gln Ala Gly Phe Ser
2540 2545 2550
Asp Glu Glu Ala Ala Arg Ser His Leu Lys Ser Leu Cys Phe Phe
2555 2560 2565
Gly Gln Ser Val Val Asn Leu Gln Glu Met Val Leu His Val Pro
2570 2575 2580
Thr Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly
2585 2590 2595
Gly Gly Gly Gly Gly Gly Gly Gly Ser Tyr His Cys Leu Ala
2600 2605 2610
Cys Glu Ser Ala Leu Cys Gly Glu Glu Ala Leu Ser Gln His Leu
2615 2620 2625
Glu Ser Ala Leu His Lys His Arg Thr Ile Thr Arg Ala Ala Arg
2630 2635 2640
Asn Ala Lys Glu His Pro Ser Leu Leu Pro His Ser Ala Cys Phe
2645 2650 2655
Pro Asp Pro Ser Thr Ala Ser Thr Ser Gln Ser Ala Ala His Ser
2660 2665 2670
Asn Asp Ser Pro Pro Pro Pro Ser Ala Ala Ala Pro Ser Ser Ala
2675 2680 2685
Ser Pro His Ala Ser Arg Lys Ser Trp Pro Gln Val Val Ser Arg
2690 2695 2700
Ala Ser Ala Ala Lys Pro Pro Ser Phe Pro Pro Leu Ser Ser Ser
2705 2710 2715
Ser Thr Val Thr Ser Ser Ser Cys Ser Thr Ser Gly Val Gln Pro
2720 2725 2730
Ser Met Pro Thr Asp Asp Tyr Ser Glu Glu Ser Asp Thr Asp Leu
2735 2740 2745
Ser Gln Lys Ser Asp Gly Pro Ala Ser Pro Val Glu Gly Pro Lys
2750 2755 2760
Asp Pro Ser Cys Pro Lys Asp Ser Gly Leu Thr Ser Val Gly Thr
2765 2770 2775
Asp Thr Phe Arg Leu
2780

```

```

<210> 15
<211> 30
<212> DNA

```

<213> Artificial

<220>

<223> synthetic

<400> 15

agatcttaag cagaaatgat tgcaccattg

30

<210> 16

<211> 28

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 16

gtagataaag gtgtgtgtca ctgagctc

28

<210> 17

<211> 19

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 17

ttggggttat tcgcaacgg

19

<210> 18

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 18

gaactggatc cctgctcata taccttgtct cgatg

35

<210> 19

<211> 26

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 19

gaactggatc caccaaggac tccatg

26

<210> 20

<211> 18

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 20
cggaattagc ttggctgc

18

cggaattagc ttggctgc